STIC-Biotech/ChemLib 75704

From: Gibbs, Terra
Sent: Friday, September 13, 2002 1:40 PM
To: STIC-Biotech/ChemLib
Subject: SEQ Search

Could you please search SEQ ID NO: 3 of serial number 10/008789

Please do a length limited search of 50 nucleotides or less. Also no EST's.

Terra Gibbs #79523
AU 1635
Mailbox 11E12
306-3221

THANK YOU!

Edward Hart
Technical Info. Specialist
STIC/Biotech
CM1 6B02 Tel: 305-9203

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 9/14/02
Date Completed: 9/18/02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 01
WWW/Internet: _____
Other (specify): _____

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 18, 2002, 00:00:48 ; Search time 2325.86 Seconds
(without alignments)
15790.319 Million cell updates/sec

Title: US-10-008-789-3
Perfect score: 1755
Sequence: 1 cgcccgggcaggtcccaaaa.....aaaaaaaaaaaaaaaaaaaa 1755

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 708260

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	30.6	1.7	48	6	AR079463	AR079463 Sequence
2	24.8	1.4	35	6	I29924	I29924 Sequence 37
3	24.8	1.4	36	6	I29930	I29930 Sequence 43
4	24.8	1.4	37	6	I29925	I29925 Sequence 38
5	24.8	1.4	41	6	I29926	I29926 Sequence 39
6	24.8	1.4	44	6	I29927	I29927 Sequence 40
c 7	24.4	1.4	40	6	AX299729	AX299729 Sequence
8	24.4	1.4	47	6	AX114342	AX114342 Sequence
9	24.4	1.4	48	6	AX166869	AX166869 Sequence
c 10	24.2	1.4	29	9	HSA241944	AJ241944 Homo sapi
11	23.8	1.4	34	6	I29923	I29923 Sequence 36
c 12	23.6	1.3	38	6	AX009602	AX009602 Sequence
c 13	23.6	1.3	45	6	I32121	I32121 Sequence 11
14	23.4	1.3	37	6	AX183756	AX183756 Sequence
c 15	23.4	1.3	42	6	AR093361	AR093361 Sequence
c 16	23.4	1.3	42	6	AR135443	AR135443 Sequence
c 17	23.4	1.3	45	6	AX172348	AX172348 Sequence
c 18	23.4	1.3	46	6	AX287577	AX287577 Sequence
c 19	23.4	1.3	46	6	AX287581	AX287581 Sequence
c 20	23.4	1.3	50	6	AX160532	AX160532 Sequence
c 21	23.2	1.3	37	9	HSOBRI05	U62489 Human OBR g
c 22	23.2	1.3	46	6	AX287579	AX287579 Sequence
c 23	23.2	1.3	46	6	AX287583	AX287583 Sequence
c 24	23.2	1.3	50	6	AX159492	AX159492 Sequence
c 25	23.2	1.3	50	6	AX159494	AX159494 Sequence
c 26	23.2	1.3	50	6	AX159496	AX159496 Sequence
c 27	23	1.3	50	9	HSTFE3IA4	X84968 H.sapiens t
28	22.8	1.3	33	6	I29922	I29922 Sequence 35
c 29	22.8	1.3	40	6	AX299730	AX299730 Sequence
c 30	22.8	1.3	45	6	AX009469	AX009469 Sequence
c 31	22.8	1.3	47	6	A25348	A25348 Synthetic m
c 32	22.8	1.3	50	6	AX261361	AX261361 Sequence
33	22.8	1.3	50	6	I36502	I36502 Sequence 1
c 34	22.6	1.3	38	6	AX009601	AX009601 Sequence
c 35	22.6	1.3	40	6	AX299737	AX299737 Sequence
36	22.4	1.3	36	6	AR099789	AR099789 Sequence
37	22.4	1.3	36	6	AR108836	AR108836 Sequence
38	22.4	1.3	36	6	AR127808	AR127808 Sequence
39	22.4	1.3	36	6	AR135337	AR135337 Sequence
40	22.4	1.3	36	6	AR152407	AR152407 Sequence
41	22.4	1.3	36	6	AR153821	AR153821 Sequence
42	22.4	1.3	36	6	AR177970	AR177970 Sequence
43	22.4	1.3	36	6	AR177974	AR177974 Sequence
44	22.4	1.3	36	6	AX041011	AX041011 Sequence
45	22.4	1.3	36	6	AX046432	AX046432 Sequence

ALIGNMENTS

RESULT 1
AR079463
LOCUS AR079463 48 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 14 from patent US 5965541.
ACCESSION AR079463
VERSION AR079463.1 GI:10006207
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 48)
AUTHORS Wickham,T.J., Kovesdi,I. and Brough,D.E.
TITLE Vectors and methods for gene transfer to cells
JOURNAL Patent: US 5965541-A 14 12-OCT-1999;
FEATURES Location/Qualifiers
source 1. .48
/organism="unknown"
BASE COUNT 30 a 4 c 6 g 8 t
ORIGIN

Query Match 1.7%; Score 30.6; DB 6; Length 48;
Best Local Similarity 80.0%; Pred. No. 2.2e+04;

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 18, 2002, 01:22:31 ; Search time 217.49 Seconds
(without alignments)
13854.360 Million cell updates/sec

Title: US-10-008-789-3
Perfect score: 1755
Sequence: 1 cgcccgggcaggtcccaaaa.....aaaaaaaaaaaaaaaaaaaa 1755

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1905168

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
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3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
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6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
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17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
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21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	28	1.6	40	22	AAH20344	HHV6 virus p41 gen
c	2	26.6	1.5	46	22	AAL28897	Human SNP oligonuc
c	3	26.4	1.5	40	22	AAH20360	HHV6 virus p41 gen
c	4	26	1.5	45	22	AAL32265	Human SNP oligonuc
	5	25.6	1.5	37	19	AAV12343	Ribonucleotide red
c	6	25.6	1.5	44	22	AAL28737	Human SNP oligonuc
	7	24.8	1.4	47	20	AAZ01118	Probe for human PG
c	8	24.6	1.4	40	22	AAH20340	HHV6 virus p41 gen
c	9	24.4	1.4	40	24	AAD22099	PCR primer, BAR-G
	10	24.4	1.4	48	22	AAD11285	Mycobacterium 16S
	11	23.8	1.4	42	20	AAZ23473	A. thaliana at-cbf
c	12	23.8	1.4	45	22	AAL28218	Human SNP oligonuc
c	13	23.8	1.4	46	22	AAL28459	Human SNP oligonuc
c	14	23.8	1.4	47	22	AAL29941	Human SNP oligonuc
c	15	23.6	1.3	38	21	AAZ43897	M. tuberculosis rp
c	16	23.6	1.3	49	22	AAL29254	Human SNP oligonuc
c	17	23.6	1.3	50	22	AAL30600	Human SNP oligonuc
	18	23.6	1.3	50	22	AAL31672	Human SNP oligonuc
	19	23.4	1.3	36	19	AAV15458	PR-1 promoter prim
	20	23.4	1.3	37	22	AAH91177	Human inflammatory
c	21	23.4	1.3	42	15	AAQ68942	Vaccinia virus lat
c	22	23.4	1.3	42	15	AAQ70569	Sequence of late p
c	23	23.4	1.3	42	18	AAT48509	Synthetic late pro
c	24	23.4	1.3	42	20	AAX81146	Synthetic FPV prom
c	25	23.4	1.3	42	21	AAC67861	Fowlpox vector syn
c	26	23.4	1.3	42	21	AAZ49294	Synthetic pox viru
c	27	23.4	1.3	45	20	AAZ31524	Probe for HIV RNA
c	28	23.4	1.3	45	20	AAZ11012	Probe #1 for HIV t
c	29	23.4	1.3	45	22	AAD18751	Probe #1 used for
c	30	23.4	1.3	46	24	AAS95730	Allele discriminat
c	31	23.4	1.3	46	24	AAS95734	Allele discriminat
c	32	23.4	1.3	50	22	AAI76919	Human silent SNP c
c	33	23.2	1.3	38	20	AAZ23096	A. thaliana gene a
	34	23.2	1.3	46	22	AAL28963	Human SNP oligonuc
c	35	23.2	1.3	46	24	AAS95732	Allele discriminat
c	36	23.2	1.3	46	24	AAS95736	Allele discriminat
	37	23.2	1.3	47	20	AAZ01041	Probe for human PG
	38	23.2	1.3	47	22	AAF89211	Sample member clus
c	39	23.2	1.3	48	20	AAX27675	Potato Lectin HRGP
c	40	23.2	1.3	50	22	AAI75879	Human silent SNP c
c	41	23.2	1.3	50	22	AAI75881	Human silent SNP c
c	42	23.2	1.3	50	22	AAI75883	Human silent SNP c
	43	23	1.3	41	24	ABA04734	Human ubiquitin-bi
c	44	23	1.3	42	22	AAH20332	Rabies virus glyco
	45	23	1.3	44	22	AAF60443	DNA oligonucleotid

ALIGNMENTS

RESULT 1
AAH20344/c
ID AAH20344 standard; DNA; 40 BP.
XX
AC AAH20344;
XX
DT 01-AUG-2001 (first entry)
XX
DE HHV6 virus p41 gene specific primer p41FH373 SEQ ID 25.
XX
KW Primer; solid phase amplification of DNA template; SPADT; detection; RGP;
KW genomic scanning; bacterial diagnostic; p41; HHV6; ss.
XX
OS Human herpesvirus 6.
OS Synthetic.
XX
PN US6221635-B1.
XX
PD 24-APR-2001.
XX
PF 06-MAY-1999; 99US-0306290.
XX
PR 06-MAY-1999; 99US-0306290.
XX
PA (WIST-) WISTAR INST.
XX
PI Rovera G, Mukhopadhyay S;
XX
DR WPI; 2001-315577/33.
XX
PT Detecting the presence of a specific nucleic acid in a sample
PT containing DNA, useful in scanning large genomic fragments for the

PT presence of genes or gene families, comprises performing solid phase
PT amplification of DNA template -
XX
PS Example 2; Column 28; 49pp; English.
XX
CC This invention relates to a method for detecting the presence of a
CC specific nucleic acid in a sample containing DNA. The method comprises
CC performing solid phase amplification of DNA template (SPADT). 5' and 3'
CC primers are irreversible bound to a solid support, and the DNA from a
CC sample is absorbed and reversibly bound, incubated under amplification
CC reaction conditions and the presence of the specific target DNA is
CC detected. The method is useful for detecting the presence of a specific
CC nucleic acid (e.g. bacterial, viral or parasitic DNA) in a sample or in a
CC cell. SPADT may be used for scanning large genomic fragments for the
CC presence of genes or gene families; or for bacterial diagnostics by
CC examining the ribosomal RNA genes; or for viral diagnostics by scanning
CC for the presence of viral nucleic acid sequences in a sample. SPADT may
CC also be used in forensic medicine by detecting and identifying species
CC specific sequences or for the presence of major histocompatibility
CC complex. The present sequence represents a primer specific for the human
CC herpesvirus 6 (HHV6) p41 gene. The primer is used in an example
CC illustrating the method of the invention.
XX
SQ Sequence 40 BP; 4 A; 2 C; 6 G; 28 T; 0 other;

Query Match 1.6%; Score 28; DB 22; Length 40;
Best Local Similarity 86.1%; Pred. No. 2e+03;
Matches 31; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1720 aatccctcgagtttacaaaaaaaaaaaaaaaaaaaa 1755
|| |||||| | || ||||||||||||||||||||
Db 36 AAACCCTCGTATATAGAAAAAAAAAAAAAAAAAAAA 1

RESULT 2
AAL28897/c
ID AAL28897 standard; DNA; 46 BP.
XX
AC AAL28897;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #2105.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
PS Claim 1; Page 1984; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
SQ Sequence 46 BP; 9 A; 4 C; 3 G; 30 T; 0 other;

Query Match 1.5%; Score 26.6; DB 22; Length 46;
Best Local Similarity 78.0%; Pred. No. 4.4e+03;
Matches 32; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1714 aataataatccctcgagtttacaaaaaaaaaaaaaaaaaa 1754
||||| || | | || ||||||||||||||||||||
Db 45 AATAAAAAGATTTTGTGTCAACAAAAAAAAAAAAAAAAAA 5

RESULT 3
AAH20360/c
ID AAH20360 standard; DNA; 40 BP.
XX
AC AAH20360;
XX
DT 01-AUG-2001 (first entry)
XX
DE HHV6 virus p41 gene specific primer HHV8RP1191 SEQ ID 41.
XX
KW Primer; solid phase amplification of DNA template; SPADT; detection; RGP;
KW genomic scanning; bacterial diagnostic; p41; HHV6; ss.
XX
OS Human herpesvirus 6.
OS Synthetic.
XX
PN US6221635-B1.
XX
PD 24-APR-2001.
XX
PF 06-MAY-1999; 99US-0306290.
XX
PR 06-MAY-1999; 99US-0306290.
XX
PA (WIST-) WISTAR INST.
XX
PI Rovera G, Mukhopadhyay S;
XX
DR WPI; 2001-315577/33.
XX
PT Detecting the presence of a specific nucleic acid in a sample
PT containing DNA, useful in scanning large genomic fragments for the
PT presence of genes or gene families, comprises performing solid phase
PT amplification of DNA template -
XX
PS Example 2; Column 28; 49pp; English.
XX
CC This invention relates to a method for detecting the presence of a
CC specific nucleic acid in a sample containing DNA. The method comprises
CC performing solid phase amplification of DNA template (SPADT). 5' and 3'

CC primers are irreversible bound to a solid support, and the DNA from a
CC sample is absorbed and reversibly bound, incubated under amplification
CC reaction conditions and the presence of the specific target DNA is
CC detected. The method is useful for detecting the presence of a specific
CC nucleic acid (e.g. bacterial, viral or parasitic DNA) in a sample or in a
CC cell. SPADT may be used for scanning large genomic fragments for the
CC presence of genes or gene families; or for bacterial diagnostics by
CC examining the ribosomal RNA genes; or for viral diagnostics by scanning
CC for the presence of viral nucleic acid sequences in a sample. SPADT may
CC also be used in forensic medicine by detecting and identifying species
CC specific sequences or for the presence of major histocompatibility
CC complex. The present sequence represents a primer specific for the human
CC herpesvirus 6 (HHV6) p41 gene. The primer is used in an example
CC illustrating the method of the invention.
XX
SQ Sequence 40 BP; 7 A; 2 C; 6 G; 25 T; 0 other;

Query Match 1.5%; Score 26.4; DB 22; Length 40;
Best Local Similarity 83.3%; Pred. No. 4.7e+03;
Matches 30; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1719 taatccctcgagtttacaaaaaaaaaaaaaaaaaaa 1754
||| ||| || || | ||||||||||||||||||||
Db 36 TAACCCCCTGATTTGAAAAAAAAAAAAAAAAAAAAA 1

RESULT 4
AAL32265/c
ID AAL32265 standard; DNA; 45 BP.
XX
AC AAL32265;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #5473.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
PS Claim 1; Page 2962; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
SQ Sequence 45 BP; 7 A; 2 C; 5 G; 31 T; 0 other;

Query Match 1.5%; Score 26; DB 22; Length 45;
Best Local Similarity 76.2%; Pred. No. 6.1e+03;
Matches 32; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1714 aataataatccctcgagtttacaaaaaaaaaaaaaaaaaaa 1755
||||| | | | |||| ||||||||||||||||||||
Db 43 AATAAACAAAACCCTAGTTCTGAAAAAAAAAAAAAAAAAAAA 2

RESULT 5
AAV12343
ID AAV12343 standard; DNA; 37 BP.
XX
AC AAV12343;
XX
DT 17-JUN-1998 (first entry)
XX
DE Ribonucleotide reductase R2 3'UTR fragment SEQ ID NO:42.
XX
KW Ribonucleotide reductase R2; 3'-untranslated region; 3'UTR; tumour;
KW housekeeping gene; identification; modulator; metastasis; neoplastic;
KW papilloma; atherosclerosis; angiogenesis; viral infection; ss.
XX
OS Homo sapiens.
XX
PN WO9800532-A2.
XX
PD 08-JAN-1998.
XX
PF 30-JUN-1997; 97WO-CA00454.
XX
PR 01-JUL-1996; 96US-0021152.
XX
PA (WRIG/) WRIGHT J A.
PA (YOUN/) YOUNG A H.
XX
PI Wright JA, Young AH;
XX
DR WPI; 1998-086958/08.
XX
PT New oligo-nucleotide(s) complementary to untranslated regions of
PT housekeeping genes - are useful in, e.g. identifying modulators of
PT tumour growth/metastasis and inhibiting growth of neoplastic cells
XX
PS Claim 7; Page 32; 64pp; English.
XX
CC The present sequence represents a 3'-untranslated region (3'UTR) fragment
CC of ribonucleotide reductase R2. The present invention describes: (1)
CC oligonucleotides (ON) comprising at least 7 consecutive nucleotides (nt)
CC or their analogues of a UTR of a housekeeping gene; (2) antisense ON
CC (AON) complementary to ON; (3) ribozymes (Rb) complementary or homologous
CC to ON, and able to cleave it; (4) DNA sequence encoding ON, OAN and Rb;
CC (5) an antibody (Ab) that binds to ON, OAN and Rb; (6) a nt probe ntP
CC that hybridise to ON, OAN and Rb. ON, AON, Rb and Ab are used to modulate
CC (especially inhibit) growth of tumour cells (especially neoplastic cells)
CC and to reduce their capacity for metastasis. The above may also be used
CC to treat benign proliferative disorders e.g. papillomas, atherosclerosis,

```
CC   angiogenesis and viral infections, e.g. human immunodeficiency virus,
CC   hepatitis or herpes. ON may further be used: (i) to identify modulators
CC   of tumour growth/metastasis; (ii) to identify compounds (especially
CC   potential antitumour agents) that inhibit or enhance interaction between
CC   ON and its binding substances; (iii) as probes for detecting related
CC   sequences, and (iv) to generate Ab, used for detection and quantification
CC   of UTR especially for monitoring progress of cancer therapy. SON inhibit
CC   tumorigenicity of neoplastic cells, particularly where these are
CC   resistant to hydroxyurea.
XX
SQ   Sequence 37 BP; 27 A; 3 C; 2 G; 5 T; 0 other;


  Query Match             1.5%;  Score 25.6;  DB 19;  Length 37;
  Best Local Similarity   87.5%;  Pred. No. 7.1e+03;
  Matches   28;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy   1724 cctcgagtttacaaaaaaaaaaaaaaaaaaa 1755
           |||  |||| | ||||||||||||||||||||
Db      2 cctgtagttcataaaaaaaaaaaaaaaaaaa 33


RESULT   6
AAL28737/c
ID   AAL28737 standard; DNA; 44 BP.
XX
AC   AAL28737;
XX
DT   24-JAN-2002  (first entry)
XX
DE   Human SNP oligonucleotide #1945.
XX
KW   Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW   neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW   amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW   cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW   complement related protein; cytochrome; kinesin; cytokine; interferon;
KW   interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW   multifactorial disease; autoimmune disease; infection;
KW   nervous system disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200147944-A2.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US35498.
XX
PR   28-DEC-1999;   99US-0173419.
PR   27-DEC-2000; 2000US-0173419.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2001-465210/50.
XX
PT   Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT   oncogenes and histones, useful for diagnosing and treating, e.g.
PT   cancer, autoimmune diseases and infections
XX
PS   Claim 1; Page 1937; 4143pp; English.
XX
CC   The present invention relates to oligonucleotides encoding polymorphic
CC   variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC   apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC   histones, kinases, colony stimulating factors, complement related
CC   proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC   G-protein coupled receptors and thioesterases. The present sequence is
CC   one such oligonucleotide. The oligonucleotides and the peptides encoded
CC   by them may be used in the prevention, diagnosis and treatment of
CC   diseases associated with inappropriate expression of the proteins listed
CC   above. Disorders that may be prevented, diagnosed and/or treated include
CC   multifactorial diseases with a genetic component, such as autoimmune
CC   diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC   systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC   (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC   leukaemia), diseases of the nervous system and an infection of pathogenic
CC   organisms.
XX
SQ   Sequence 44 BP; 11 A; 1 C; 4 G; 28 T; 0 other;


  Query Match             1.5%;  Score 25.6;  DB 22;  Length 44;
  Best Local Similarity   77.5%;  Pred. No. 7.6e+03;
  Matches   31;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   1716 taataatccctcgagtttacaaaaaaaaaaaaaaaaaaa 1755
           || |||  ||   | |||  ||||||||||||||||||||
Db     41 TATTAAATCCAGTATTTTCAAAAAAAAAAAAAAAAAAA 2


RESULT   7
AAZ01118
ID   AAZ01118 standard; DNA; 47 BP.
XX
AC   AAZ01118;
XX
DT   27-SEP-1999  (first entry)
XX
DE   Probe for human PG1 biallelic marker 4-4-187.
XX
KW   PG1 gene; biallelic marker; PCR primer; PG1-related biallelic marker;
KW   cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
KW   PSA; human; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9932644-A2.
XX
PD   01-JUL-1999.
XX
PF   22-DEC-1998;   98WO-IB02133.
XX
PR   09-SEP-1998;   98US-0099658.
PR   22-DEC-1997;   97US-0996306.
XX
PA   (GEST ) GENSET.
XX
PI   Blumenfeld M,  Bougueleret L,  Chumakov I,  Cohen D;
XX
DR   WPI; 1999-405178/34.
XX
PT   Use of a prostate cancer associated gene and biallelic markers
PT   derived from it
XX
PS   Claim 4; Page 325; 385pp; English.
XX
CC   The invention relates to a mammalian PG1 gene and protein, and a set of
CC   PG1 biallelic markers. The PG1 polynucleotide and biallelic markers are
CC   used in a hybridisation assay, a sequencing assay, or in an
CC   allele-specific amplification assay for determining the identity of a
CC   nucleotide at a PG1-related biallelic marker. The methods can be used to
CC   detect and to assess the risk of developing cancer or prostate cancer.
CC   Early-stage diagnosis of prostate cancer relies on prostate specific
CC   antigen (PSA) dosage. However, the effectiveness of this is limited due
CC   to its inability to discriminate between malignant and non-malignant
CC   affections of the organ. A need exists for both a reliable diagnostic
CC   procedure which would enable early-stage diagnosis, and for preventative
CC   and curative treatments of the disease. The PG1 gene can be used for
CC   detection of prostate cancer, and the risk of developing it in the
CC   future, and can also be used to determine therapies for the disease.
XX
SQ   Sequence 47 BP; 34 A; 2 C; 5 G; 6 T; 0 other;
```

```
  Query Match             1.4%;  Score 24.8;  DB 20;  Length 47;
  Best Local Similarity   92.9%;  Pred. No. 1.2e+04;
  Matches   26;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy   1728 gagtttacaaaaaaaaaaaaaaaaaaaa 1755
          ||||| | ||||||||||||||||||||
Db     20 gagttaaaaaaaaaaaaaaaaaaaaaaa 47


RESULT   8
AAH20340/c
ID   AAH20340 standard; DNA; 40 BP.
XX
AC   AAH20340;
XX
DT   01-AUG-2001  (first entry)
XX
DE   HHV6 virus p41 gene specific primer p41FH92 SEQ ID 21.
XX
KW   Primer; solid phase amplification of DNA template; SPADT; detection; RGP;
KW   genomic scanning; bacterial diagnostic; p41; HHV6; ss.
XX
OS   Human herpesvirus 6.
OS   Synthetic.
XX
PN   US6221635-B1.
XX
PD   24-APR-2001.
XX
PF   06-MAY-1999;   99US-0306290.
XX
PR   06-MAY-1999;   99US-0306290.
XX
PA   (WIST-) WISTAR INST.
XX
PI   Rovera G,  Mukhopadhyay S;
XX
DR   WPI; 2001-315577/33.
XX
PT   Detecting the presence of a specific nucleic acid in a sample
PT   containing DNA, useful in scanning large genomic fragments for the
PT   presence of genes or gene families, comprises performing solid phase
PT   amplification of DNA template -
XX
PS   Example 2; Column 28; 49pp; English.
XX
CC   This invention relates to a method for detecting the presence of a
CC   specific nucleic acid in a sample containing DNA. The method comprises
CC   performing solid phase amplification of DNA template (SPADT). 5' and 3'
CC   primers are irreversible bound to a solid support, and the DNA from a
CC   sample is absorbed and reversibly bound, incubated under amplification
CC   reaction conditions and the presence of the specific target DNA is
CC   detected. The method is useful for detecting the presence of a specific
CC   nucleic acid (e.g. bacterial, viral or parasitic DNA) in a sample or in a
CC   cell. SPADT may be used for scanning large genomic fragments for the
CC   presence of genes or gene families; or for bacterial diagnostics by
CC   examining the ribosomal RNA genes; or for viral diagnostics by scanning
CC   for the presence of viral nucleic acid sequences in a sample. SPADT may
CC   also be used in forensic medicine by detecting and identifying species
CC   specific sequences or for the presence of major histocompatibility
CC   complex. The present sequence represents a primer specific for the human
CC   herpesvirus 6 (HHV6) p41 gene. The primer is used in an example
CC   illustrating the method of the invention.
XX
SQ   Sequence 40 BP; 9 A; 2 C; 4 G; 25 T; 0 other;


  Query Match             1.4%;  Score 24.6;  DB 22;  Length 40;
  Best Local Similarity   76.9%;  Pred. No. 1.3e+04;
  Matches   30;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   1717 aataatccctcgagtttacaaaaaaaaaaaaaaaaaaa 1755
          |||| |    |   ||| ||||||||||||||||||||
Db     40 AATAGTTTTCCAGCTTTTCAAAAAAAAAAAAAAAAAAA 2


RESULT   9
AAD22099/c
ID   AAD22099 standard; DNA; 40 BP.
XX
AC   AAD22099;
XX
DT   12-FEB-2002  (first entry)
XX
DE   PCR primer, BAR-G used for haplotyping hybridisation.
XX
KW   Human; Haplotype determination; single nucleotide polymorphism; SNP1;
KW   PL1; polymorphic locus; insulin-dependent diabetes mellitus; IDDM;
KW   multiple sclerosis; Alzheimer's disease; eye colour; asthma; cancer;
KW   neurofibromatosis type 2; cystic fibrosis; thalassaemia; phenylketonuria;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "Amidated thymidine"
XX
PN   WO200175163-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US10173.
XX
PR   04-APR-2000; 2000US-194425P.
XX
PA   (POLY-) POLYGENYX INC.
XX
PI   Landers JE;
XX
DR   WPI; 2002-010802/01.
XX
PT   Haplotyping comprises separately analyzing first and second alleles of
PT   first and second single nucleotide polymorphisms of two different
PT   polymorphic loci, and determining haplotype based on each allele
PT   identification -
XX
PS   Example 2; Page 41; 77pp; English.
XX
CC   The patent discloses high throughput methods for determining haplotypes.
CC   Haplotyping comprises analysing first and second alleles of a first
CC   single nucleotide polymorphism (SNP1) of a first polymorphic locus
CC   (PL1) by specifically capturing the nucleic acid sample on a surface,
CC   separately analysing a second SNP of a polymorphic locus of a nucleic
CC   acid sample to identify both alleles of SNP2, and determining the
CC   haplotype based on the identification of each allele of each SNP.
CC   The method is useful for haplotyping a nucleic acid within a sample.
CC   It is useful for screening DNA to identify polymorphic haplotypes,
CC   and identification of haplotypes associated with predisposition to
CC   diseases as well as other genetically associated traits. SNP haplo-
CC   typing is useful in linkage disequilibrium studies for the analysis
CC   of complex traits to localised genes involved in diseases such as
CC   insulin-dependent diabetes mellitus (IDDM), multiple sclerosis,
CC   Alzheimer's disease and asthma, diagnostic analysis to determine
CC   the presence or absence of a predisposing disease haplotype or
CC   other trait, pharmacogenomic analysis to identify haplotypes that
CC   correlates with either positive or negative responses to drugs and
CC   development, genome-wide scan studies for complex trait analysis using
CC   SNP haplotypes, instead of single SNPs to increase the statistical
CC   power. The methods of the invention are useful for identifying both
CC   normal phenotypes and disease phenotypes. They are useful for the
CC   identification of traits such as eye colour and for diagnostics to
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CC   determine presence or absence of predisposing disease haplotypes
CC   such as colon cancer, breast cancer, neurofibromatosis type 2,
CC   cystic fibrosis, thalassaemia and phenylketonuria. Identification
CC   of haplotypes associated with phenotypic traits is useful for
CC   identifying predisposition to disease. The methods are also useful
CC   in prenatal screening to identify whether a foetus is afflicted
CC   with or is predisposed to develop a serious disease. The present
CC   DNA sequence is PCR primer, BAR-G used for haplotyping hybridisation
CC   in the exemplification of the invention.
XX
SQ   Sequence 40 BP; 6 A; 6 C; 3 G; 25 T; 0 other;


  Query Match             1.4%;  Score 24.4;  DB 24;  Length 40;
  Best Local Similarity   82.4%;  Pred. No. 1.4e+04;
  Matches   28;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   1722 tcccctcgagtttacaaaaaaaaaaaaaaaaaaaa 1755
            ||| | | ||  | ||||||||||||||||||||
Db     34 TCCATTGGGTGAAAAAAAAAAAAAAAAAAAAAA 1


RESULT  10
AAD11285
ID   AAD11285 standard; DNA; 48 BP.
XX
AC   AAD11285;
XX
DT   24-SEP-2001  (first entry)
XX
DE   Mycobacterium 16S rRNA capture oligomer.
XX
KW   Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
KW   Mycobacterium other than tuberculosis; MOTT; capture oligomer; ss.
XX
OS   Mycobacterium sp.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag= a
FT                    /mod_base= cm
FT   modified_base    2
FT                    /*tag= b
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxy-thymidine"
FT   modified_base    3
FT                    /*tag= c
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxy-adenosine"
FT   modified_base    4
FT                    /*tag= d
FT                    /mod_base= gm
FT   modified_base    5
FT                    /*tag= e
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxy-thymidine"
FT   modified_base    6
FT                    /*tag= f
FT                    /mod_base= cm
FT   modified_base    7
FT                    /*tag= g
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxy-thymidine"
FT   modified_base    8
FT                    /*tag= h
FT                    /mod_base= gm
FT   modified_base    9..11
FT                    /*tag= i
FT                    /mod_base= cm
FT   modified_base    12
FT                    /*tag= j
FT                    /mod_base= gm
FT   modified_base    13
FT                    /*tag= k
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxy-thymidine"
FT   modified_base    14
FT                    /*tag= l
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxy-adenosine"
FT   modified_base    15
FT                    /*tag= m
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methoxy-thymidine"
XX
PN   WO200144510-A2.
XX
PD   21-JUN-2001.
XX
PF   17-DEC-1999;   99WO-US30346.
XX
PR   17-DEC-1999;   99WO-US30346.
XX
PA   (GENP-) GEN-PROBE INC.
PA   (INMR ) BIOMERIEUX SA.
XX
PI   Brentano ST,  Jucker MT,  Delgado FD,  Cleuziat P,  Rodrigue M;
XX
DR   WPI; 2001-398170/42.
XX
PT   Detecting Mycobacterium species, involves in vitro amplification of 16S
PT   rRNA or DNA encoding RNA in nucleic acid amplification mixture using
PT   specific primers, and detecting the amplified nucleic acid
XX
PS   Example 6; Page 39; 44pp; English.
XX
CC   The invention relates to a method of detecting Mycobacterium species,
CC   that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
CC   encoding 16S rRNA in an in vitro nucleic acid amplification mixture
CC   comprising a polymerase, and at least two primers, and then detecting
CC   the amplified nucleic acid. The method is relatively simple and useful
CC   for detecting the presence of various Mycobacterium species in a
CC   biological sample, and thus important for diagnosis of infections
CC   resulting from them. The method is especially important for screening
CC   opportunistic infections caused by M. tuberculosis or a Mycobacterium
CC   other than tuberculosis (MOTT). The present sequence is a capture
CC   oligomer that includes a sequence that specifically binds to the
CC   Mycobacterium rRNA target sequence and a 3' poly-A tail sequence
CC   complementary to an immobilised sequence for capturing the target rRNA
CC   on a solid support.
XX
SQ   Sequence 48 BP; 32 A; 5 C; 3 G; 8 T; 0 other;


  Query Match             1.4%;  Score 24.4;  DB 22;  Length 48;
  Best Local Similarity   82.4%;  Pred. No. 1.5e+04;
  Matches   28;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   1722 tcccctcgagtttacaaaaaaaaaaaaaaaaaaaa 1755
            | ||   | |||| ||||||||||||||||||||
Db      7 tgcccgtattttaaaaaaaaaaaaaaaaaaaa 40


RESULT  11
AAZ23473
ID   AAZ23473 standard; DNA; 42 BP.
XX
AC   AAZ23473;
XX
DT   20-JAN-2000  (first entry)
XX
DE   A. thaliana at-cbf1 gene PCR primer cbf1-forward 1.
XX
KW   Environmental stress tolerance; plant; binding protein; DNA regulation;
KW   CBF-1; C-repeat/DRE binding factor; CCG regulatory sequence; COR; cold;
KW   cold-related gene; drought; high salinity; tissue-specific promoter;
```

KW PCR primer; at-cbf1; ss.
XX
OS Synthetic.
OS Arabidopsis thaliana.
XX
PN WO9938977-A2.
XX
PD 05-AUG-1999.
XX
PF 28-JAN-1999; 99WO-US01895.
XX
PR 03-FEB-1998; 98US-0017575.
PR 03-FEB-1998; 98US-0017816.
PR 03-FEB-1998; 98US-0018227.
PR 03-FEB-1998; 98US-0018233.
PR 03-FEB-1998; 98US-0018234.
PR 03-FEB-1998; 98US-0018235.
PR 23-NOV-1998; 98US-0198119.
XX
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
PA (UNMS) UNIV MICHIGAN STATE.
XX
PI Stockinger EJ, Jaglo-Ottosen K, Zarka D, Gilmour SJ, Jiang C;
PI Fromm M, Thomashow MF;
XX
DR WPI; 1999-561312/47.
XX
PT Environmental stress tolerance gene binding proteins useful for
PT altering plant stress tolerance -
XX
PS Example 4c; Page 181; 252pp; English.
XX
CC This invention describes novel binding proteins other than CBF-1
CC (C-repeat/DRE binding factor) in isolated form which comprise a
CC consensus sequence capable of binding to a CCG regulatory sequence.
CC The binding proteins are capable of binding to a DNA regulatory
CC sequence, which regulates expression of one or more environmental
CC stress tolerance genes, especially COR (cold-related) genes.
CC Environmental stress may be, e.g. cold temperatures, drought and high
CC salinity. Plants transformed with the binding protein (or sequences
CC encoding it) can have altered environmental stress tolerance. The
CC binding protein coding sequences can be under the control of
CC tissue-specific promoters. AA23472-23475 represent PCR primers used
CC in the amplification of the Arabidopsis thaliana at-cbf1 gene described
CC in the method of the invention.
XX
SQ Sequence 42 BP; 18 A; 9 C; 5 G; 10 T; 0 other;

```
  Query Match             1.4%;  Score 23.8;  DB 20;  Length 42;
  Best Local Similarity   80.0%;  Pred. No. 2e+04;
  Matches   28;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy    1721 atccctcgagtttacaaaaaaaaaaaaaaaaaaa 1755
           ||||||||  | ||||| || |||| |||| ||||
Db       6 atccctcgtttctacaacaataaaataaaataaaa 40
```

RESULT 12
AAL28218/c
ID AAL28218 standard; DNA; 45 BP.
XX
AC AAL28218;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #1426.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
PS Claim 1; Page 1788; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
SQ Sequence 45 BP; 8 A; 4 C; 3 G; 30 T; 0 other;

```
  Query Match             1.4%;  Score 23.8;  DB 22;  Length 45;
  Best Local Similarity   92.6%;  Pred. No. 2.1e+04;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    1729 agtttacaaaaaaaaaaaaaaaaaaaa 1755
           | ||||||||||  ||||||||||||||
Db      30 AATTTACAAAAATAAAAAAAAAAAAAA 4
```

RESULT 13
AAL28459/c
ID AAL28459 standard; DNA; 46 BP.
XX
AC AAL28459;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #1667.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;

```
KW   nervous system disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200147944-A2.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US35498.
XX
PR   28-DEC-1999;   99US-0173419.
PR   27-DEC-2000; 2000US-0173419.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2001-465210/50.
XX
PT   Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT   oncogenes and histones, useful for diagnosing and treating, e.g.
PT   cancer, autoimmune diseases and infections -
XX
PS   Claim 1; Page 1857; 4143pp; English.
XX
CC   The present invention relates to oligonucleotides encoding polymorphic
CC   variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC   apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC   histones, kinases, colony stimulating factors, complement related
CC   proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC   G-protein coupled receptors and thioesterases. The present sequence is
CC   one such oligonucleotide. The oligonucleotides and the peptides encoded
CC   by them may be used in the prevention, diagnosis and treatment of
CC   diseases associated with inappropriate expression of the proteins listed
CC   above. Disorders that may be prevented, diagnosed and/or treated include
CC   multifactorial diseases with a genetic component, such as autoimmune
CC   diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC   systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC   (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC   leukaemia), diseases of the nervous system and an infection of pathogenic
CC   organisms.
XX
SQ   Sequence 46 BP; 4 A; 3 C; 3 G; 36 T; 0 other;


  Query Match             1.4%;  Score 23.8;  DB 22;  Length 46;
  Best Local Similarity   92.6%;  Pred. No. 2.1e+04;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    1729 agtttacaaaaaaaaaaaaaaaaaaaaa 1755
           | || ||||||||||||||||||||||
Db      27 AATTAACAAAAAAAAAAAAAAAAAAAAA 1


RESULT  14
AAL29941/c
ID   AAL29941 standard; DNA; 47 BP.
XX
AC   AAL29941;
XX
DT   24-JAN-2002  (first entry)
XX
DE   Human SNP oligonucleotide #3149.
XX
KW   Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW   neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW   amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW   cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW   complement related protein; cytochrome; kinesin; cytokine; interferon;
KW   interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW   multifactorial disease; autoimmune disease; infection;
KW   nervous system disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200147944-A2.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US35498.
XX
PR   28-DEC-1999;   99US-0173419.
PR   27-DEC-2000; 2000US-0173419.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2001-465210/50.
XX
PT   Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT   oncogenes and histones, useful for diagnosing and treating, e.g.
PT   cancer, autoimmune diseases and infections -
XX
PS   Claim 1; Page 2289; 4143pp; English.
XX
CC   The present invention relates to oligonucleotides encoding polymorphic
CC   variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC   apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC   histones, kinases, colony stimulating factors, complement related
CC   proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC   G-protein coupled receptors and thioesterases. The present sequence is
CC   one such oligonucleotide. The oligonucleotides and the peptides encoded
CC   by them may be used in the prevention, diagnosis and treatment of
CC   diseases associated with inappropriate expression of the proteins listed
CC   above. Disorders that may be prevented, diagnosed and/or treated include
CC   multifactorial diseases with a genetic component, such as autoimmune
CC   diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC   systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC   (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC   leukaemia), diseases of the nervous system and an infection of pathogenic
CC   organisms.
XX
SQ   Sequence 47 BP; 10 A; 4 C; 2 G; 31 T; 0 other;


  Query Match             1.4%;  Score 23.8;  DB 22;  Length 47;
  Best Local Similarity   92.6%;  Pred. No. 2.1e+04;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    1729 agtttacaaaaaaaaaaaaaaaaaaaaa 1755
           || | ||||||||||||||||||||||
Db      28 AGCTAACAAAAAAAAAAAAAAAAAAAAA 2


RESULT  15
AAZ43897/c
ID   AAZ43897 standard; DNA; 38 BP.
XX
AC   AAZ43897;
XX
DT   10-MAR-2000  (first entry)
XX
DE   M. tuberculosis rpo-beta primer 10.
XX
KW   RNA polymerase; rpo-beta; detection; diagnostic; trap probe; primer; ss.
XX
OS   Mycobacterium tuberculosis.
XX
PN   EP962536-A1.
XX
PD   08-DEC-1999.
XX
PF   29-MAY-1999;   99EP-0110458.
XX
PR   04-JUN-1998;   98DE-1024900.
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XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Weindel K, Brand J;
XX
DR WPI; 2000-055287/05.
XX
PT Selective detection of nucleic acids by amplification with labeled
PT primers and detection with a trap probe
XX
PS Example 1c; Page 18; 27pp; German.
XX
CC This invention describes a novel method for the selective detection of
CC nucleic acids which comprises amplification of the nucleic acid with the
CC help of labeled primers and detection with a trap probe. The methods and
CC reagents are used for the detection of a marker primer and at least 2
CC immobilized (or immobilizable) trap probes with the corresponding nucleic
CC acid sequence of interest for mutation analysis. The method can be used
CC to detect a specific sequence in a sample of one or more nucleic acids by
CC using several sets of primers and trap probes (i.e. in an array). The
CC methods are useful in molecular biology and diagnostic applications,
CC especially for simultaneous detection of multi-pathogens, typing of
CC organisms, analyzing genetic diversity and sequencing of genes or
CC genomes. This sequence represents a primer used in the method of the
CC invention.
XX
SQ Sequence 38 BP; 4 A; 7 C; 5 G; 22 T; 0 other;

Query Match 1.3%; Score 23.6; DB 21; Length 38;
Best Local Similarity 86.7%; Pred. No. 2.2e+04;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1726 tcgagtttacaaaaaaaaaaaaaaaaaaa 1755
||| | || ||||||||||||||||||||
Db 30 TCGGGGTTGAAAAAAAAAAAAAAAAAAAA 1

Search completed: September 18, 2002, 03:33:04
Job time: 7833 sec